

# Genome-wide association study of normal tension glaucoma: common variants in SRBD1 and ELOVL5 contribute to disease susceptibility

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## Abstract

**PURPOSE:** Factors contributing to the development of normal tension glaucoma (NTG), degenerative optic neuropathy characterized by the progressive loss of retinal ganglion cells, optic nerve axons, and visual fields, have not been determined. To identify genetic risk factors for NTG, we performed a genome-wide association study of NTG.

**DESIGN:** Case-control study.

**PARTICIPANTS:** The study cohort consisted of 305 Japanese patients with NTG and 355 controls.

**METHODS:** We genotyped 500,568 single-nucleotide polymorphisms (SNPs) and assessed the allelic diversity among cases and controls.

**MAIN OUTCOME MEASURES:** Genotypes of 500,568 SNPs.

**RESULTS:** The 2 most strongly NTG-associated SNPs, rs3213787 and rs735860, are located in an intron of SRBD1 and the 3'-untranslated region of ELOVL5 ( $P = 2.5 \times 10^{-9}$ ), odds ratio = 2.80 and  $P = 4.1 \times 10^{-6}$ , odds ratio = 1.69), respectively. Real-time quantitative reverse transcription-polymerase chain reaction assays showed significantly increased expression of each gene in the white blood cells of subjects harboring the risk allele of these SNPs.

**CONCLUSIONS:** Our genome-wide association study identified SRBD1 and ELOVL5 as new susceptibility genes for NTG. Because SRBD1 and ELOVL5 are reportedly involved in the induction of cell growth inhibition or apoptosis, the regulation of SRBD1 and ELOVL5 cascades may play an important physiologic role in the risk of NTG development.

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